

SEQUENCE LISTING

<110> Payne, Jewel
Sick, August J.

<120> Novel *Bacillus thuringiensis* Isolate Active Against Lepidopteran
Pests, and Genes Encoding Novel Lepidopteran-Active Toxins

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<151> 2001-04-19

<150> US 09/521,344
<151> 2000-03-09

<150> US 08/933,891
<151> 1997-09-19

<150> US 08/356,034
<151> 1994-12-14

<150> US 08/210,110
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<150> US 07/865,168
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<150> US 371,955
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<170> PatentIn version 3.2

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 Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu Gln Leu
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 Asp Val His Arg Gly Phe Asn Tyr Trp Ser Gly His Gln Ile Thr Ala
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<213> *Bacillus thuringiensis*

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 Leu Gly Thr Leu Arg Val Thr Phe Thr Gly Arg Leu Pro Gln Ser Tyr
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 Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe
 515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met
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Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu
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Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln Glu Glu Phe Asp Leu Tyr
 565 570 575

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr
 580 585 590

Ala Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Val Val
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Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr Asp Val
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Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Ala Cys Leu Ser
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Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys
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His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
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Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr
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Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
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Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
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Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
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Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
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Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp
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Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg
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Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg
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Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
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Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
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Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
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Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys
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Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu
 865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
 885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met
 900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu
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Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
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Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
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Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val
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Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
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Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
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Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly
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Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr
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Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro
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Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu
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Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala
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Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr
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Glu Glu Lys Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu
 1100 1105 1110

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
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Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp
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Glu Leu Leu Leu Met Glu Glu
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| agtagcgggtg | aacttttat | agataaaatt | gaaattattc | tagcagatgc | aacatttgaa | 1860 |
| gcagaatctg | atttagaaa | agcacaaaag | gcggtgaatg | ccctgtttac | ttcttccaat | 1920 |
| caaatecggt | taaaaaccga | tgtgacggat | tatcatattg | atcaagtatc | caatttagtg | 1980 |
| gattgtttat | cagatgaatt | ttgtctggat | gaaaagcgag | aattgtccga | gaaagtcaaa | 2040 |
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| gacgtattca | aagagaatta | cgtcacacta | ccgggtaccg | ttgatgagtg | ctatccaacg | 2220 |
| tatttatatc | agaaaataga | tgagtcgaaa | ttaaaagctt | ataccctgta | tgaattaaga | 2280 |
| gggtatatcg | aagatagtca | agacttagaa | atctatttga | tcggttacia | tgcaaaacac | 2340 |
| gaaatagtaa | atgtgccagg | cacgggttcc | ttatggccgc | tttcagccca | aagtccaatc | 2400 |
| ggaaagtgtg | gagaaccgaa | tcgatgcgcg | ccacaccttg | aatggaatcc | tgatctagat | 2460 |
| tgttcctgca | gagacgggga | aaaatgtgca | catcattccc | atcatttcac | cttgatatt | 2520 |
| gatgttggat | gtacagactt | aaatgaggac | ttaggtctat | gggtgatatt | caagattaag | 2580 |
| acgcaagata | accatgcaag | actagggat | ctagagtttc | tcgaagagaa | accattatta | 2640 |
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| ctgcagttgg | aaacaaatat | tgtttataaa | gaggcaaaag | aatctgtaga | tgctttattt | 2760 |
| gtaaactctc | aatatgatag | attacaagtg | aatacgaaca | tcgcaatgat | tcatgcggca | 2820 |
| gataaacgcg | ttcatagaat | ccgggaagcg | tatctgccag | agttgtctgt | gattccaggt | 2880 |
| gtcaatgcgg | ccattttcga | agaattagag | ggacgtattt | ttacagcgta | ttccttatat | 2940 |
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| aaaggtcatg | tagatgtaga | agagcaaaac | aaccaccgtt | cggtccttgt | tatcccagaa | 3060 |
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| aatacagacg | aactgaaatt | cagcaactgt | gtagaagagg | aagtatatcc | aaacaacaca | 3240 |
| gtaacgtgta | ataattatac | tgggactcaa | gaagaatatg | agggtacgta | cacttctcgt | 3300 |
| aatcaaggat | atgacgaagc | ctatggtaat | aacccttcg | taccagctga | ttacgcttca | 3360 |
| gtctatgaag | aaaaatcgta | tacagatgga | cgaagagaga | atccttgtga | atctaacaga | 3420 |

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Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
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Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
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Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
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Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
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Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
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Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
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Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
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Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
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Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
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Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
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Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
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Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
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Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
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Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
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Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
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Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
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Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
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Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
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Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
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Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365

Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
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Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400

Arg Gly Arg Gly Gln Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
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Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
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Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
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Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
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Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
 465 470 475 480

Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
 485 490 495

Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
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Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
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Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
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Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
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Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
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Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
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Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
 595 600 605

Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
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Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
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Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
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Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
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Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
 675 680 685

Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
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Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
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Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
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Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
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Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
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Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
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Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 785 790 795 800

Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
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Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
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Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845

Glu Asp Leu Gly Leu Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Asn
 850 855 860

His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880

Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 885 890 895

Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910

Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
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Gln Val Asn Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
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His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 945 950 955 960

Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
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Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 980 985 990

Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005

Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala
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Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
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Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val
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Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
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Ser Arg Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser
 1100 1105 1110

Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr
 1115 1120 1125

Asp Gly Arg Arg Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly
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Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu
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Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr
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Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu
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| actcgacaat gggcaagatt caatcagttt aggagagatt taacacttac tgtattagat | 720 |
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| tccgagaaag tcaaacatgc gaagcgactc agtgatgagc ggaatttact tcaagatcca | 2040 |
| aacttcaaag gcatcaatag gcaactagac cgtggttgga gaggaagtac ggatattacc | 2100 |
| atccaaagag gagatgacgt attcaaagaa aattatgtca cactaccagg tacctttgat | 2160 |

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<212> PRT

<213> *Bacillus thuringiensis*

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Asn Pro Glu Val Glu Ile Leu Asn Glu Glu Arg Ser Thr Gly Arg Leu
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Pro Leu Asp Ile Ser Leu Ser Leu Thr Arg Phe Leu Leu Ser Glu Phe
 35 40 45

Val Pro Gly Val Gly Val Ala Phe Gly Leu Phe Asp Leu Ile Trp Gly
 50 55 60

Phe Ile Thr Pro Ser Asp Trp Ser Leu Phe Leu Leu Gln Ile Glu Gln
 65 70 75 80

Leu Ile Glu Gln Arg Ile Glu Thr Leu Glu Arg Asn Arg Ala Ile Thr
 85 90 95

Thr Leu Arg Gly Leu Ala Asp Ser Tyr Glu Ile Tyr Ile Glu Ala Leu
 100 105 110

Arg Glu Trp Glu Ala Asn Pro Asn Asn Ala Gln Leu Arg Glu Asp Val
 115 120 125

Arg Ile Arg Phe Ala Asn Thr Asp Asp Ala Leu Ile Thr Ala Ile Asn
 130 135 140

Asn Phe Thr Leu Thr Ser Phe Glu Ile Pro Leu Leu Ser Val Tyr Val
 145 150 155 160

Gln Ala Ala Asn Leu His Leu Ser Leu Leu Arg Asp Ala Val Ser Phe
 165 170 175

Gly Gln Gly Trp Gly Leu Asp Ile Ala Thr Val Asn Asn His Tyr Asn
 180 185 190

Arg Leu Ile Asn Leu Ile His Arg Tyr Thr Lys His Cys Leu Asp Thr
 195 200 205

Tyr Asn Gln Gly Leu Glu Asn Leu Arg Gly Thr Asn Thr Arg Gln Trp
 210 215 220

Ala Arg Phe Asn Gln Phe Arg Arg Asp Leu Thr Leu Thr Val Leu Asp
 225 230 235 240

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Ile Val Ala Leu Phe Pro Asn Tyr Asp Val Arg Thr Tyr Pro Ile Gln
      245                      250                      255

Thr Ser Ser Gln Leu Thr Arg Glu Ile Tyr Thr Ser Ser Val Ile Glu
      260                      265                      270

Asp Ser Pro Val Ser Ala Asn Ile Pro Asn Gly Phe Asn Arg Ala Glu
      275                      280                      285

Phe Gly Val Arg Pro Pro His Leu Met Asp Phe Met Asn Ser Leu Phe
      290                      295                      300

Val Thr Ala Glu Thr Val Arg Ser Gln Thr Val Trp Gly Gly His Leu
      305                      310                      315                      320

Val Ser Ser Arg Asn Thr Ala Gly Asn Arg Ile Asn Phe Pro Ser Tyr
      325                      330                      335

Gly Val Phe Asn Pro Gly Gly Ala Ile Trp Ile Ala Asp Glu Asp Pro
      340                      345                      350

Arg Pro Phe Tyr Arg Thr Leu Ser Asp Pro Val Phe Val Arg Gly Gly
      355                      360                      365

Phe Gly Asn Pro His Tyr Val Leu Gly Leu Arg Gly Val Ala Phe Gln
      370                      375                      380

Gln Thr Gly Thr Asn His Thr Arg Thr Phe Arg Asn Ser Gly Thr Ile
      385                      390                      395                      400

Asp Ser Leu Asp Glu Ile Pro Pro Gln Asp Asn Ser Gly Ala Pro Trp
      405                      410                      415

Asn Asp Tyr Ser His Val Leu Asn His Val Thr Phe Val Arg Trp Pro
      420                      425                      430

Gly Glu Ile Ser Gly Ser Asp Ser Trp Arg Ala Pro Met Phe Ser Trp
      435                      440                      445

Thr His Arg Ser Ala Thr Pro Thr Asn Thr Ile Asp Pro Glu Arg Ile
      450                      455                      460

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Thr Gln Ile Pro Leu Val Lys Ala His Thr Leu Gln Ser Gly Thr Thr
 465 470 475 480

Val Val Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr
 485 490 495

Ser Gly Gly Pro Phe Ala Tyr Thr Ile Val Asn Ile Asn Gly Gln Leu
 500 505 510

Pro Gln Arg Tyr Arg Ala Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu
 515 520 525

Arg Ile Tyr Val Thr Val Ala Gly Glu Arg Ile Phe Ala Gly Gln Phe
 530 535 540

Asn Lys Thr Met Asp Thr Gly Asp Pro Leu Thr Phe Gln Ser Phe Ser
 545 550 555 560

Tyr Ala Thr Ile Asn Thr Ala Phe Thr Phe Pro Met Ser Gln Ser Ser
 565 570 575

Phe Thr Val Gly Ala Asp Thr Phe Ser Ser Gly Asn Glu Val Tyr Ile
 580 585 590

Asp Arg Phe Glu Leu Ile Pro Val Thr Ala Thr Phe Glu Ala Glu Tyr
 595 600 605

Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ile
 610 615 620

Asn Gln Ile Gly Ile Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln
 625 630 635 640

Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu
 645 650 655

Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp
 660 665 670

Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Lys Gly Ile Asn Arg Gln
 675 680 685

Leu Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Arg Gly
 690 695 700

Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp
 705 710 715 720

Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu
 725 730 735

Lys Pro Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln
 740 745 750

Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val
 755 760 765

Asn Val Leu Gly Thr Gly Ser Leu Trp Pro Leu Ser Val Gln Ser Pro
 770 775 780

Ile Arg Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp
 785 790 795 800

Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His
 805 810 815

His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu
 820 825 830

Asn Glu Asp Leu Asp Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp
 835 840 845

Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu
 850 855 860

Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg
 865 870 875 880

Asp Lys Arg Glu Lys Leu Glu Leu Glu Thr Asn Ile Val Tyr Lys Glu
 885 890 895

Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Gln
 900 905 910

Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg
 915 920 925

Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro
 930 935 940

Gly Val Asn Val Asp Ile Phe Glu Glu Leu Lys Gly Arg Ile Phe Thr
 945 950 955 960

Ala Phe Phe Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe
 965 970 975

Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu
 980 985 990

Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala
 995 1000 1005

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile
 1010 1015 1020

Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val
 1025 1030 1035

Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser
 1040 1045 1050

Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys
 1055 1060 1065

Asn Asp Tyr Thr Ala Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr
 1070 1075 1080

Ser Arg Asn Arg Gly Tyr Asp Glu Thr Tyr Gly Ser Asn Ser Ser
 1085 1090 1095

Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr
 1100 1105 1110

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly
 1115 1120 1125

Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu
 1130 1135 1140

Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr
 1145 1150 1155

Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu
 1160 1165 1170

Glu

<210> 9
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 42-mer oligonucleotide constructed to the sequence of the insert
 in pM2,31-4

<400> 9
 ggataccggt gaccattaa cattccaatc ttttagttac gc 42

<210> 10
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 40-mer oligonucleotide constructed to the sequence of the insert
 in pM2,31-1

<400> 10
 gaagtttatg gcctctttct gtagaaaatc aaattggacc 40